

ATATTGCTGAGCTCAGGAGAGTGAGGGCCCCACATTGTGACACAGTGAGCCCCAAGAAGAGG	60
GATCCCTGCTCCAGCAGCTGCAAGGTGCAAGAAGAAGAATCCACGGGAGGAAAATGTG	120
<u>H C</u>	2
CTGGAGACCCCTGTGTCGGTTCCTGTGGCTTTGGTCCTATCTGTCTTATGTTCACAGCT	180
<u>N R E L C R F L N L M S Y L S Y V Q A V</u>	22
GCCTATCCAGAAAGTCCAGGATGACACCAAACCCCTCATCAAGACCATTTGTCACCGAT	240
<u>P I Q K V Q D D T K T L I K T I V T R I</u>	210
CAATTGACATTTACACACGGCTGGTATCCGCCAAGCAGAGGGTCACTGGCTTGGACTT	300
<u>N D I S H T Q S V S A K Q R V T G L D F</u>	62
CATTCTGGGCTTCAACCCCATCTGAGTTTGTCCAAGATGGACAGACTCTGGCAGCTTA	360
<u>I P G L H P I L S L S L G K G Q C T L A V Y</u>	82
TCAACAGGTCTCTACCAGCCTGCCCTCCCAAAATGTCTGCAGATGCCAATGACCTGGA	420
<u>Q Q V L L T S L P S Q N V L Q I A N D L E</u>	102
GAATCTCCGAGAGCTCTCTCATCTGCTGGCCCTTCTCCAAGAGTGCTCCCTGCTCAGAC	480
<u>N L R D L L H L L L A F S S C S L P Q T</u>	122
CAGTGGCCTCGCAAGCCACAGAGCCTGGATGGCTCCTGGAAGCCTCACTCTACTCCAC	540
<u>S G L Q K P E S L D G V L E A S L Y S T</u>	142
AGAGTGGTGCCTTTCAGAGGCTCGAGGGCTCTCTGCAGGACATTTTCAACGATTGGA	600
<u>E V V A L L S R L Q G S L Q D I L Q Q L D</u>	162
TGTTAGCCCTGAATGTGCAAGTTTCAAAGGCCACACGGCTCCCAAGATCATGTAGAGGG	660
<u>V S P E C *</u>	167
AAGAAACCTTGGCTTCCAGGGGTCTTCAGGAGAAGAGAGCCATGTGCACACATCCATCAT	720
TCATTTCTCTCCCTCCTGTAGACCACCCATCCAAAGGCATGACTCCACAATGCTTGACTC	780
AAGTTATCCACACAACCTCATGAGCACAAAGGAGGGGCCAGCCTGCAGAGGGGACTCTCAC	840
CTAGTTCTTTCAGCAAGTAGAGATAAGAGGCATCCCATCCCCCTCATGTCCACCTGCTCC	900
GGGTACATGTTCTCCGTGGGTACACGGCTTCGCTCGGGCCACAGGAGGTCAGGTAGGGA	960
TGGGTAGAGCCTTTGGGCTGTCTCAGAGCTTTTGGGAGCACCGTGAAGGCTGCATCCACA	1020
CACAGCTGGAACCTCCCAAGCAGCACACAGATGGAAGCACTTATTTATTTATCTGCATT	1080
TATTTTGGATGGATCTGAAGCAAGGCATCAGCTTTTTCAGGCTTTGGGGGTCAAGCAGGA	1140
TGAGGAAGGCTCCTCGGGTCTGCTTTCAATCCTATTGATGGCTTCCCCGAGGCAAAAC	1200
TAATTTTTCAGTGACTGGAAGGAAGGTTGGGATCTTCCAAACAAGAGTCTATGCAGGTAG	1260
CGCTCAAGATTGACCTCTGGTGACTGGTTTGTGTTCTATTGTGACTGACTCTATCCAAAC	1320
ACGTTTGCAGCGGCAATGCGGGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTT	1380
TGTCAAAGTGTAATATGTATCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGT	1440
GAAGGATCCGGAAGTGTTCTCTGAATATACATATGTGTGGTAGGCTTTTCTGAAAGGGTG	1500
GGCATTTTCTTACCTCTGTGGCCACATAGTGTGGCTTTGTGAAAAGGACAAAGGAGTTGA	1560
CTCTTTCGGGAACATTTGGAGTGTACCAGGCCACCTTGGAGGGGCTAAAGCTACAGGCCT	1620
TTTGTGGCATAATTGCTGAGCTCAGGAGTGAGGGGCCCCACATTTACAGACAGTGAGCC	1680
AAGAAAAGGGTCCCTGGTGTGATCTCCAAAGTTGTCCAGGCTTGATCTCAACAATCGGTT	1740
TCTTAAGCAGGTAGACCTTTGCATGCCAAATGTGTGGTTTTCAGCTTGTATCTCAACAAT	1800
AGTTAGAACCCTGTCTCCCAACCATTTCTGTGGGAGTTTTGTTCCAGTGGGAATGACAAAT	1860
CAGTTAGCAGATGCTCTGAGCCCTGGGCAGCACTGCTGAGGAAGTCCAGGGGCCCCAG	1920
CCCAGGCTGCCAGAAATGCCCTTCGGGCTGGAGGATGAACAAAGGGGCTTGGGTTTTTC	1980
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GTCTTCAACAGGTGTGAAAGAACTTGAGCTGAGGGTGACAGTGCCACAGGGGAACCTGCT	2280
TGCAGTCTATTGCAATACATACCGCATTTTCAGGGCATTAGCATCCACTCCTATGGTA	2340
GCACACTGTTGCAATAGGACAAGGGATAGGGGTTGACTATCCCTTATCCAAAATGCTTG	2400
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AAAATGAGATATCTTGGCGATGGCGCCCAAGTATAAAACATGAAGTTCATTATATTTTCAT	2520
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GCATGAAGAAGCTTTTACAGCATGAACCTGCTACTACTGCCAGCACTCAAAAACCTTG	2640
GGGTTTTGAGCAGTTTGCATCTTCGGTTTCTGTTAAGAGATGGTTAGCTTATACCTAA	2700
AACCAATTCGGCAACAGCTCGAGGACAGCACTGGATCTCAGCCCTGAAGTGTGGCCT	2760
TCCAGCAAGGTCATACCTCTGAGGAGGTGAGCGGGATCAGGTTTTGTGGTGCTAAGCAGAGG	2820
TTGTGAGGTTAGATTTTGGAGGATCTGAGGGC	2852

Figure 2

---	G--	GTTG	CAAGGCCCAA	GAAGCCCA--	-TCCTGGGAA	GGAAAATGCA	50
TTGGGGAACC	CTGTG-CGGA	TTCTTGTGGC	TTTGGCCCTA	TCTTTTCTAT			100
GTCCAAGCTG	TGCCCATCCA	AAAAGTCCAA	GATGACACCA	AAACCCTCAT			150
CAAGACAATT	GTCACCAGGA	TCAATGACAT	TTCACACACG	CAGTCAGTCT			200
CCTCCAAACA	GAAAGTCACC	GGTTTGGACT	TCATTCTG	GCTCCACCCC			250
ATCCTGACCT	TATCCAAGAT	GGACCAGACA	CTGGCAGTCT	ACCAACAGAT			300
CCTCACCAGT	ATGCCTTCCA	GAAACGTGAT	CCAAATATCC	AACGACCTGG			350
AGAACCTCCG	GGATCTTCTT	CACGTGCTGG	CCTTCTCTAA	GAGCTGCCAC			400
TTGCCCTGGG	CCAGTGGCCT	GGAGACCTTG	GACAGCCTGG	GGGGTGTCTT			450
GGAAGCTTCA	GGCTACTCCA	CAGAGGTGGT	GGCCCTGAGC	AGGCTGCAGG			500
GGTCTCTGCA	GGACATGCTG	TGGCAGCTGG	ACCTCAGCCC	TGGGTGCTGA			550
GGCCTTGAAG	GTCACTCTTC	CTGCAAGGAC	T-ACGTTAAG	GGAAGGAACT			600
CTGGTTTCCA	GGTATCTCCA	GGATTGAAGA	GCATTGCATG	GACACCCCTT			650
ATCCAGGACT	CTGTCAATTT	CCCTGACTCC	TCTAAGCCAC	TCTTCCAAAG			700
G							701

```

1      Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr
16     Leu Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
31     Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile
46     Ser His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu
61     Asp Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met
76     Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro
91     Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg
106    Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro
121    Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu
136    Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu
151    Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro
166    Gly Cys End

```

Mouse	MCWRPLCRFL	WLWSYLSYVQ	AVPIQKVQDD	TKTLIKTIVT	RINDISHTQS	50
	* * *	* *				
Human	MHWGTLCGFL	WLWPYLFYVQ	AVPIQKVQDD	TKTLIKTIVT	RINDISHTQS	
Mouse	VSAKQRTVGL	DFIPGLHPIL	SLSKMDQTLA	VYQQVLTSLP	SQNVLQIAND	100
	*		-	-	* *	
Human	VSSKQKVTGL	DFIPGLHPIL	TLISKMDQTLA	VYQQILTSMP	SRNVIQISND	
Mouse	LENLRDLLHL	LAFSKSCSLP	QTSGLQKPES	LDGVLEASLY	STEVVALSRL	150
	-	*	** ***-	* *		
Human	LENLRDLLHV	LAFSKSCHLP	WASGLETLDS	LGGVLEASGY	STEVVALSRL	
Mouse	QGSLQDILQQ	LDVSPEC				167
	- *	- *				
Human	QGSLQDMLWQ	LDLSPGC				

# Figure 5

1 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr  
 16 Leu Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp  
 31 Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile  
 46 Ser His Thr Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp  
 61 Phe Ile Pro Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp  
 76 Gln Thr Leu Ala Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser  
 91 Gln Asn Val Leu Gln Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp  
 106 Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys Ser Leu Pro Gln  
 121 Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val Leu Glu  
 136 Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln  
 151 Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro Glu  
 166 Cys End

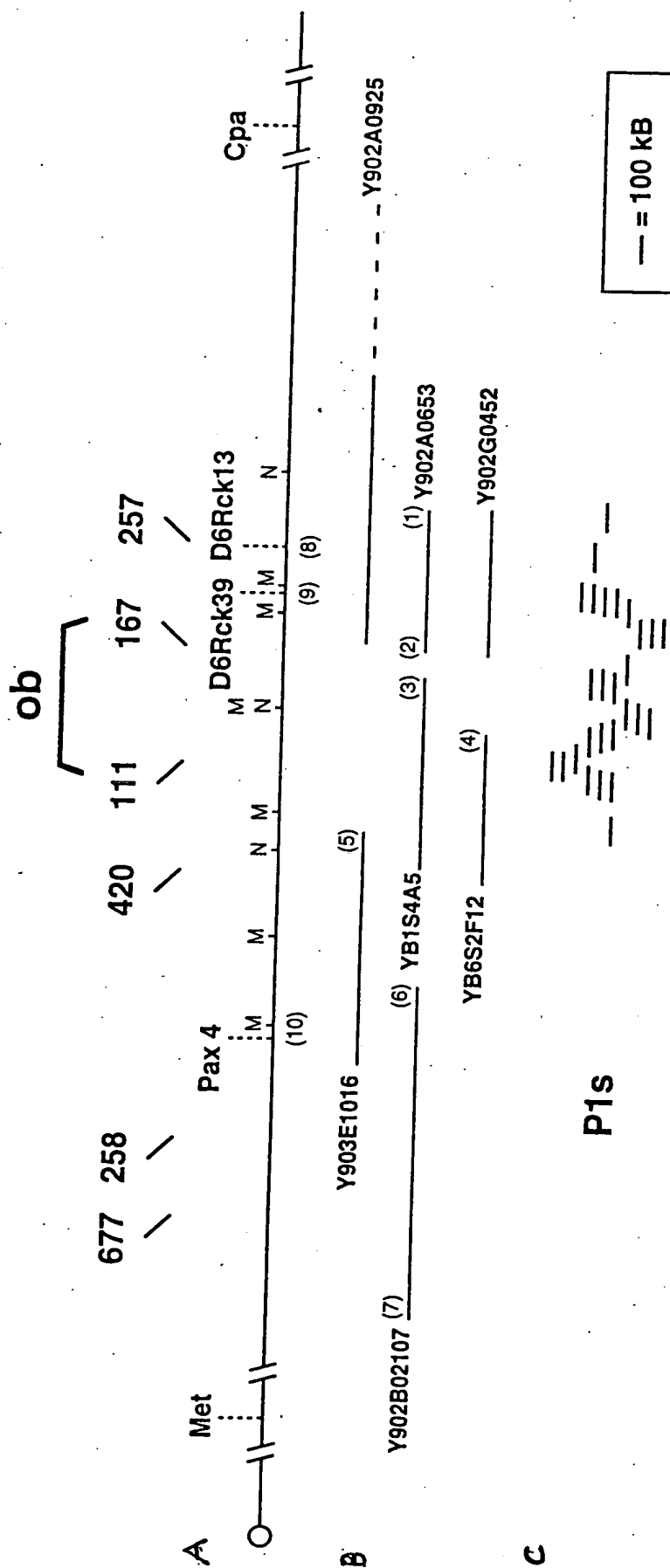
000780"49852960

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1 Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr
16 Leu Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
31 Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile
46 Ser His Thr Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp
61 Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp
76 Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser
91 Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp
106 Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp
121 Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu Glu
136 Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln
151 Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro Gly
166 Cys End

```

Figure 7



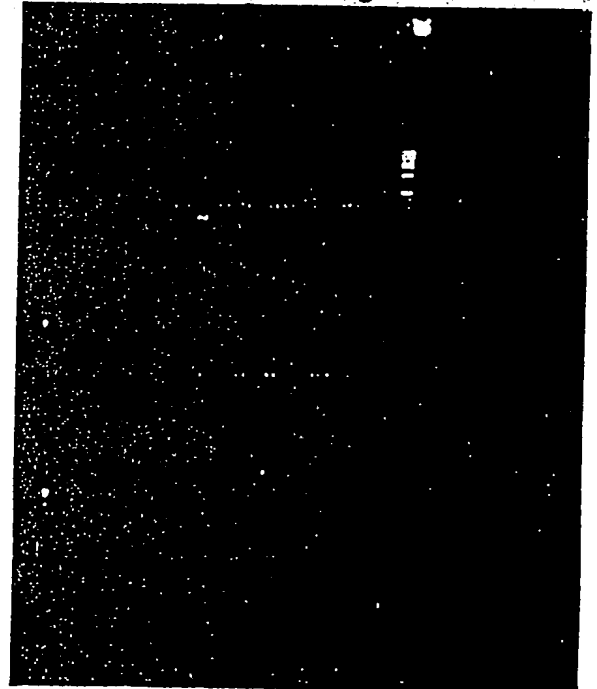
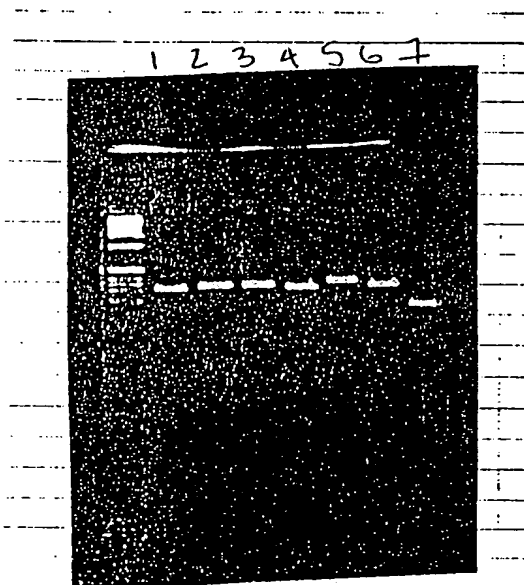


Figure 9



000780-49855960

Figure 10

+10 +20 +30 +40  
 1 GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTGCTG GAGACCCCTG  
 CACGTTCTTC TTCTTCTAGG GTCCCCTCCT TTTACACGAC CTCTGGGGAC  
 +10 +20 +30 +40  
 51 TGTCGGGTCC NGTGGNTTGG GTCCTATCTG TCTTATGTNC AAGCAGTGCC  
 ?-?-?-?-?-?-?-?-?-?  
 ACAGCCCAGG NCACCNAAC CAGGATAGAC AGAATACANG TTCGTCACGG  
 +10 +20 +30 +40  
 101 TATCCAGAAA GTCCAGGATG ACACCAAAAG CCTCATCAAG ACCATTGTCA  
 ATAGGTCTTT CAGGTCCTAC TGTGGTTTTT GGAGTAGTTC TGGTAACAGT  
 +10 +20 +30 +40  
 NCAGGATCAC TGANATTTCA CACACG  
 151 ?-?-?-?-?-?-?-?-?-?  
 NGTCCTAGTG ACTNTAAAGT GTGTGC

000780-49855960

Figure 11A

Actin →

2G7 →



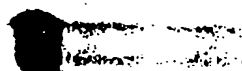
Adrenal  
Brain  
Fat  
S. Int.  
Hypoth.  
Kidney  
Lung  
Liver  
Pancreas  
Spleen  
Stomach

09635864.081000

Figure 11B

185 —

285 —



white fat

brain

small intestine

stomach

pancreas

lung

testis

heart

spleen

liver

09635864.081000

Figure 12A

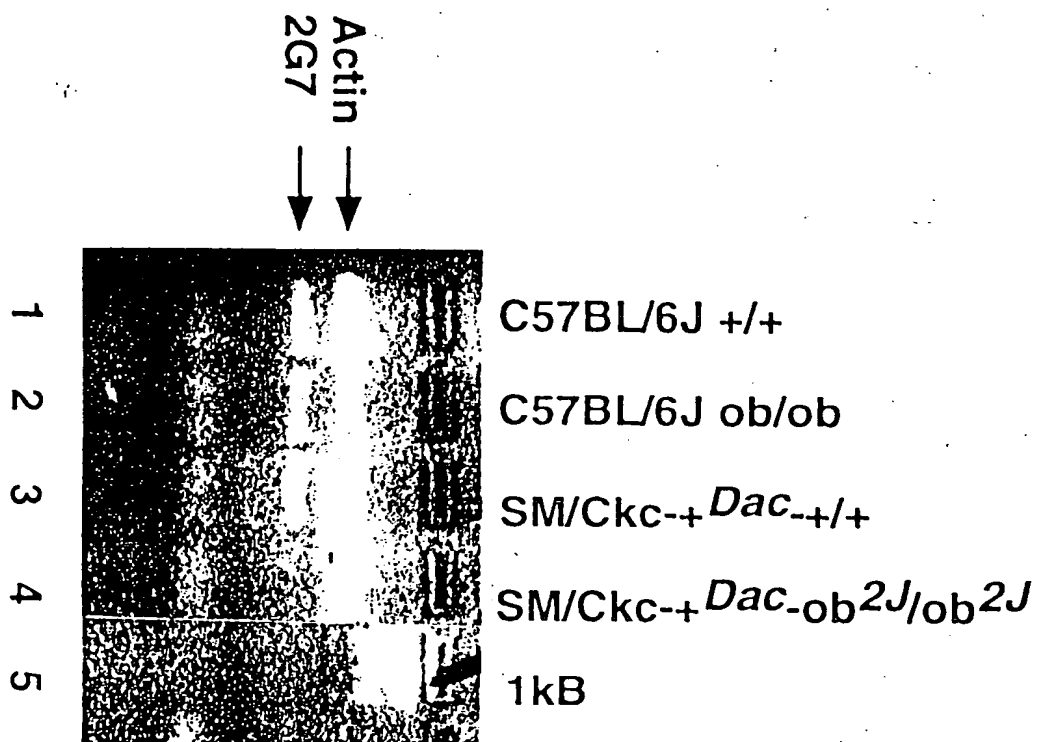
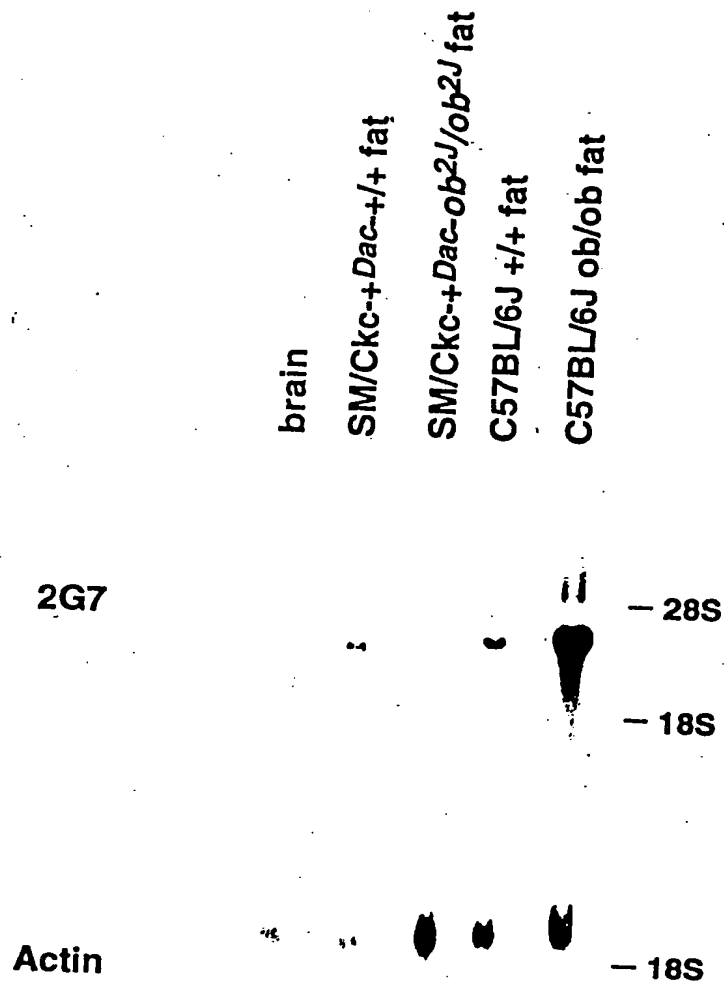


Figure 12 B



000T80" 1985E960

CKC/smj ob/ob

CKC/smj +/-

CKC/smj ob/ob

CKC/smj +/-

CKC/smj ob/ob

CKC/smj +/-

CKC/smj +/-

A high-contrast, black and white image showing a row of five dark, rectangular objects, possibly film frames or sprocket holes, against a light, textured background. The objects are arranged horizontally and appear to be part of a larger sequence or film strip. The background has a grainy, speckled texture.

Figure 14

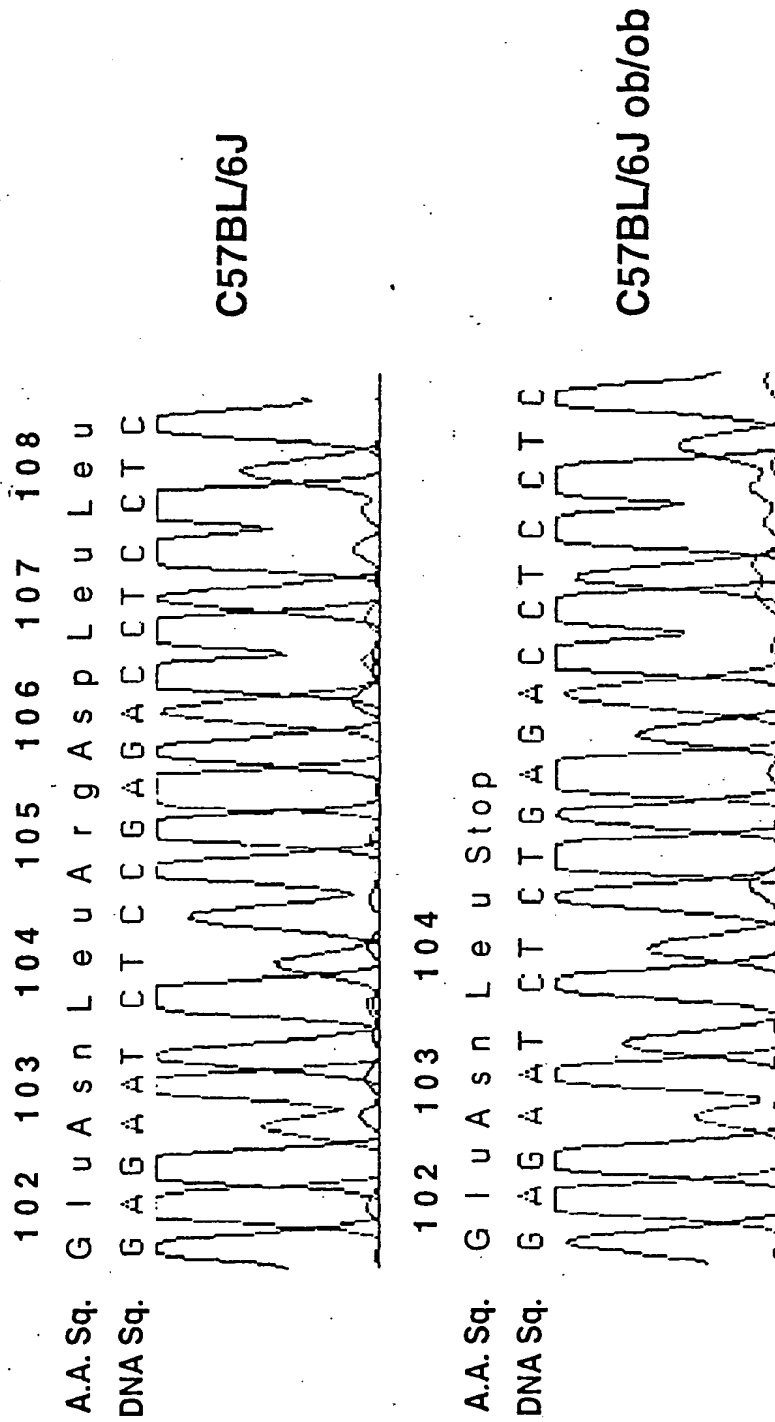


Figure 15A

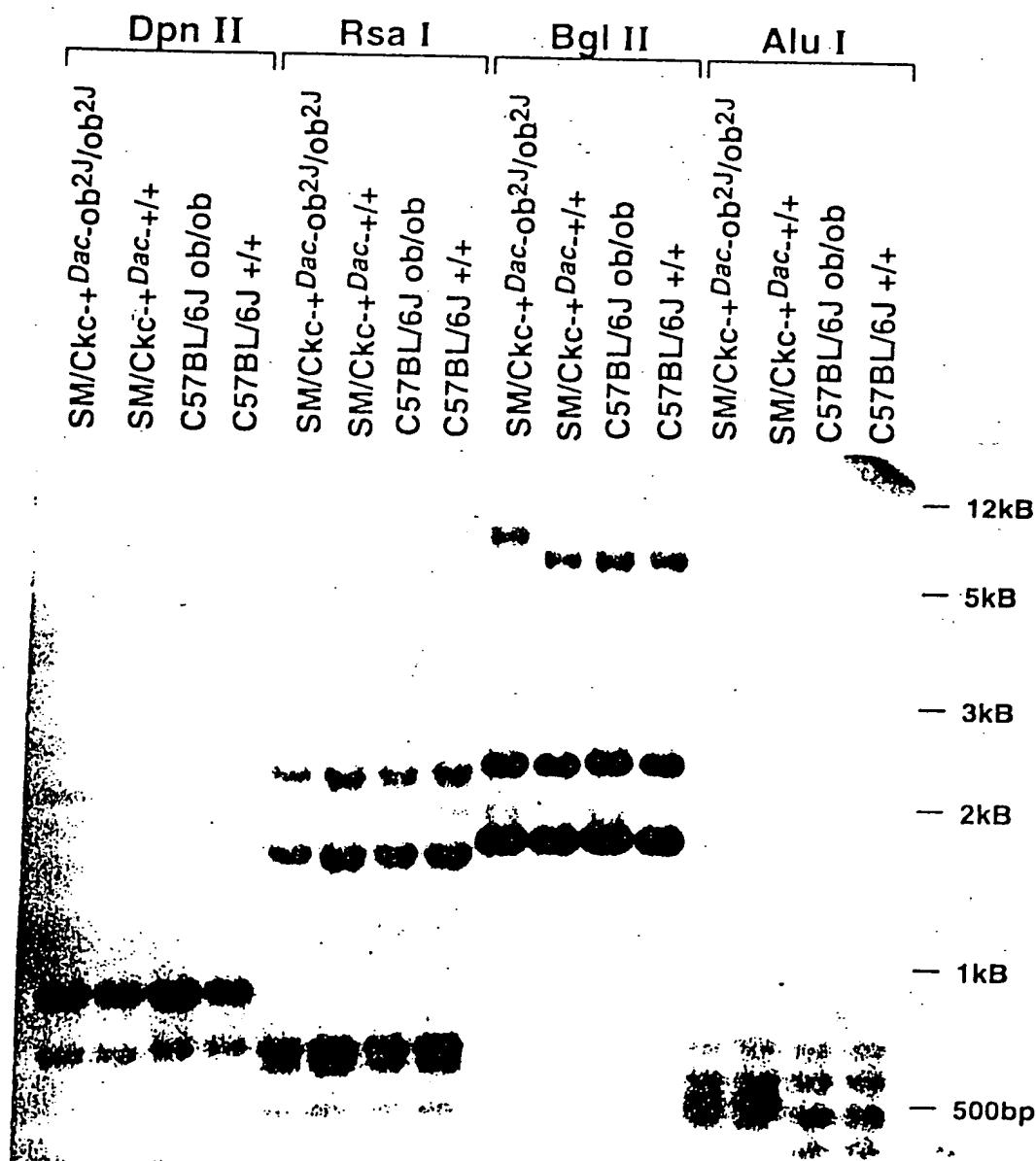


Figure 15B

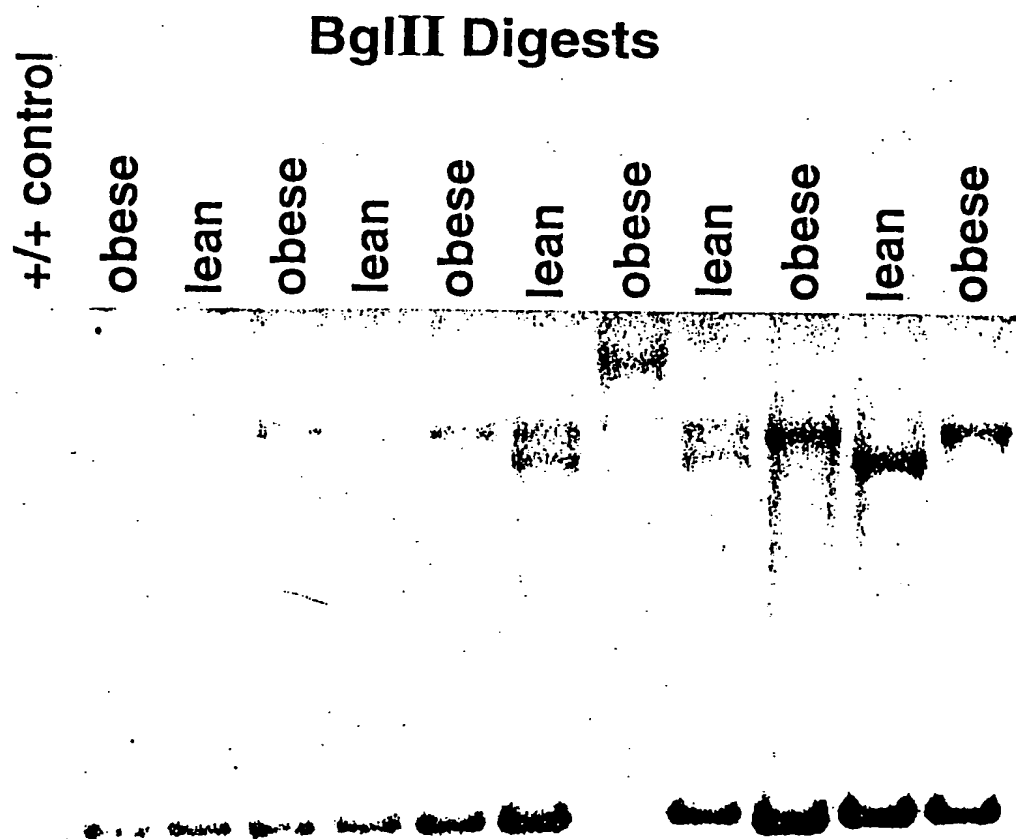
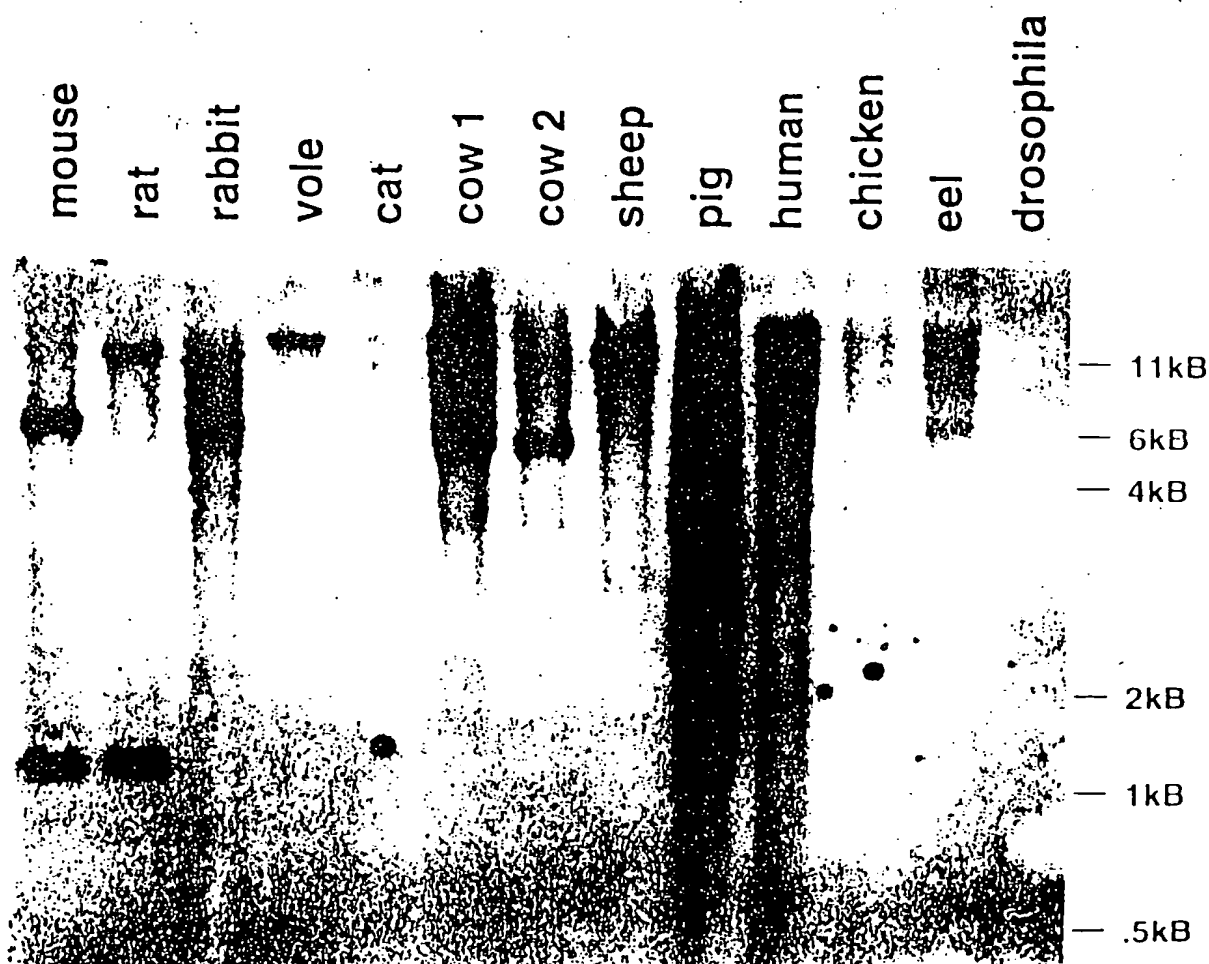
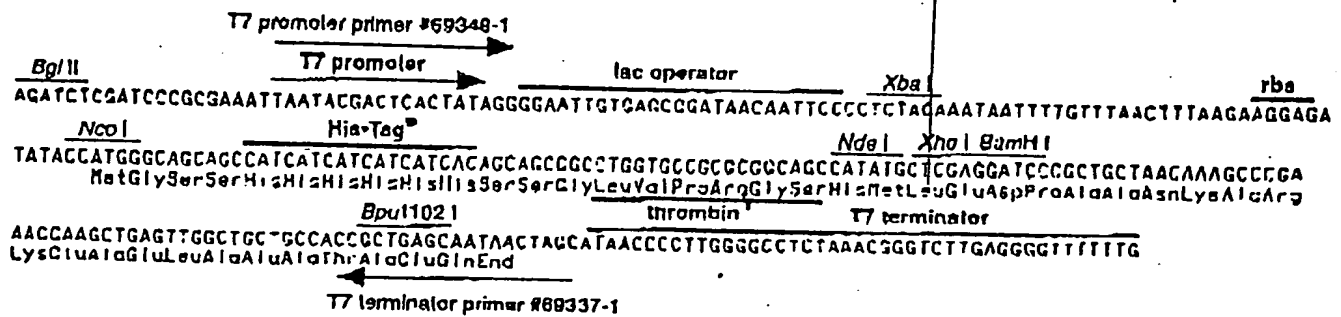


Figure 16



000T80"4985E960

Figure 17



09635864-081000

Figure 18A

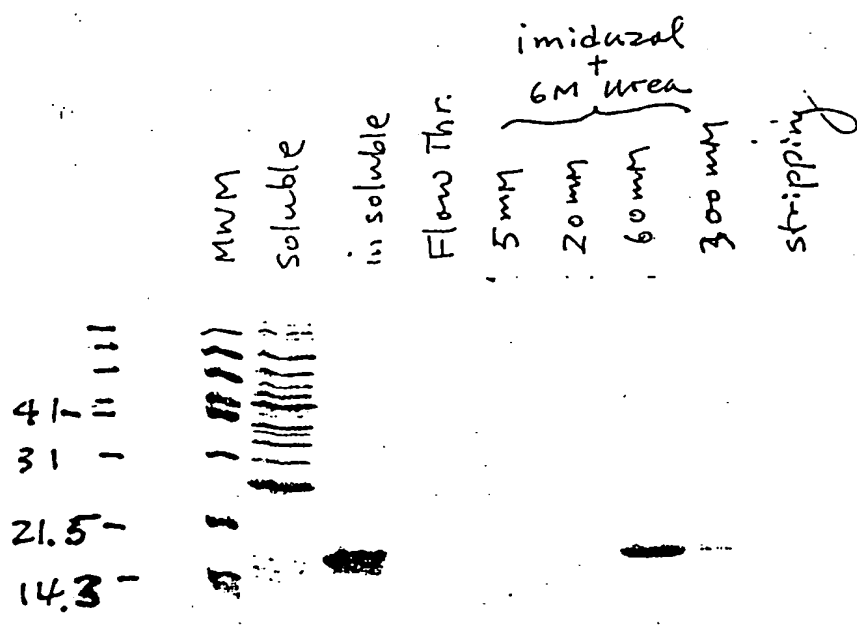


Figure 18B

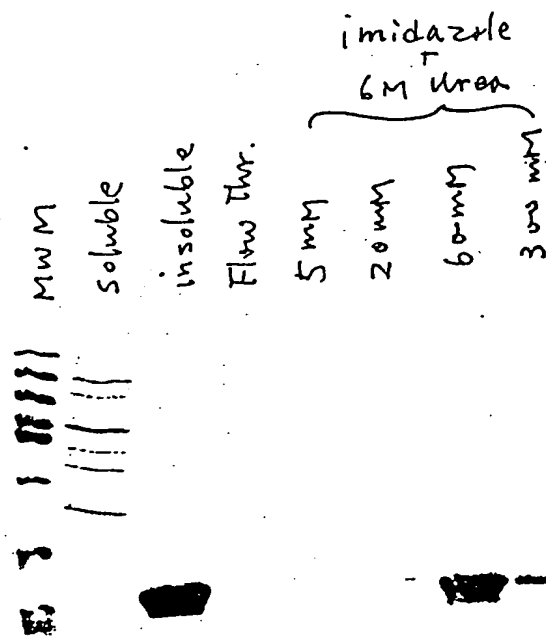
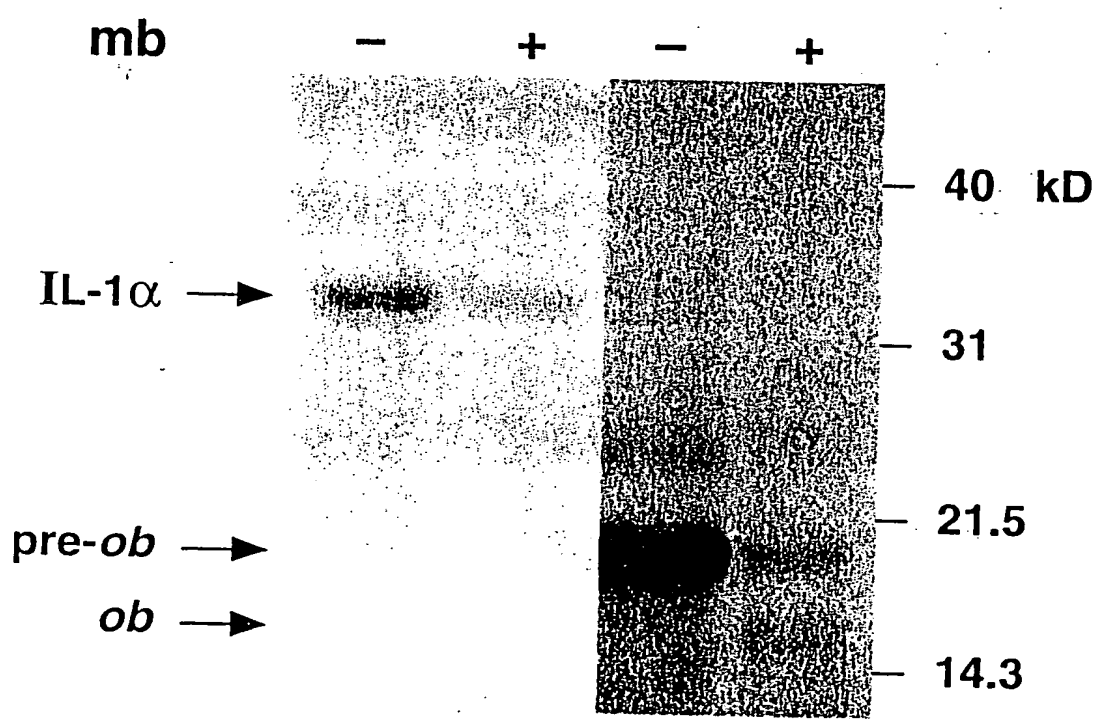


Figure 11A



000T80-4985E960

<b>Triton X-100</b>	—	—	—	—	+
<b>Proteinase K</b>	—	—	+	+	+
<b>Microsome</b>	—	+	—	+	+



Figure 20A

10	20	30	40	50
GGTTGCAAGG CCCAAGAAGC CCATCCTGGG AAGGAAATG CATTGGGGAA				
60	70	80	90	100
CCCTGTGCGG ATTCTTGTGG CTTGGCCCT ATCTTTTCTA TGTCCAAGCT				
110	120	130	140	150
GTGCCCATCC AAAAAGTCCA AGATGACACC AAAACCTCA TCAAGACAAT				
160	170	180	190	200
TGTCACCAGG ATCAATGACA TTACACACAC GGTAAAGGAGA GTATGCGGGG				
210	220	230	240	250
ACAAAGTAGA ACTGCAGCCA GCCCAGCACT GGCTCCTAGT GGCACCTGGAC				
260	270	280	290	300
CCAGATAGTC CAAGAAACAT TTATTGAACG CCTCCTGAAT GCCAGGCACC				
310	320	330	340	350
TACTGCAAGC TGAGAAGGAT TTTGGATAGC ACAGGGCTCC ACTCTTCTG				
360	370	380	390	400
GTTGTTTCT NTGGCCCCCT CTGCCTGCTG AGATNCCAGG GGTTAGNGGT				
410	420	430	440	450
TCTTAATTCC TAAA <del>WAS GAP OF SEQUENCE (~1.4 kb)</del> CT				
460	470	480	490	500
GGTTCTTTCA GGAAGAGGCC ATGTAAGAGA AAGGAATTGA CCTAGGGAAA				
510	520	530	540	550
ATTGGCCTGG GAACTGGAGG GAACGGATGG TGTGGGAAAA GCAGGAATCT				
560	570	580	590	600
CGGAGACCAG CTTAGAGGCT TGGCAGTCAC CTGGGTGCAG GANACAAGGG				
610	620	630	640	650
CCTGAGCCAA AGTGGTGAGG GAGGGTGGAA GGAGACAGCC CAGAGAATGA				
660	670	680	690	700
CCCTCCATGC CCACGGGGAA GGCAGAGGC TCTGAGAGCG ATTCTCCCA				
710	720	730	740	750
CATGCTGAGC ACTTGTTCTC CCTCTTCCTC CTNCATAGCA GTCAGTCTCC				
760	770	780	790	800
TCCAAACAGA AAGTCACCGG TTTGGACTTC ATTCTGGGC TCCACCCCAT				
810	820	830	840	850
CCTGACCTTA TCCAAGATGG ACCAGACACT GGCAGTCTAC CAACAGATCC				
860	870	880	890	900
TCACCAGTAT GCCTTCAGA AACGTGATCC AAATATCCAA CGACCTGGAG				

910	920	930	940	950
AACCTCCGGG ATCTTCTTCA CGTGCTGGCC TTCTTAAGA GCTGCCACTT				
960	970	980	990	1000
GCCCTGGGcC AGTGGCCTGG ACACCTTGA CAGCCTGGGG GGTGTCCTGG				
1010	1020	1030	1040	1050
AAGCTTCAGG CTACTCCACA GAGGTGGTGG CCCTGAGCAG GCTGCAGGGG				
1060	1070	1080	1090	1100
TCTCTGCAGG ACATGCTGTG GCAGCTGGAC CTCAGCCCTG GGTGCTGAGG				
1110	1120	1130	1140	1150
CCTTGAAGGT CACTCTTCTT GCAAGGACTA CGTTAAGGGA AGGAACCTCTG				
1160	1170	1180	1190	1200
GCTTCCAGGT ATCTCCAGGA TTGAAGAGCA TTGCATGGAC ACCCCTTATC				
1210	1220	1230	1240	1250
CAGGACTCTG TCAATTTCCC TGACTCCTCT AAGCCACTCT TCCAAGG				

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093334-081000

[illegible]

Figure 20c

..... 1st exon 1st intr 2nd exon  
.....ATG.....//.....TGA.....  
start stop

09-7684-081000

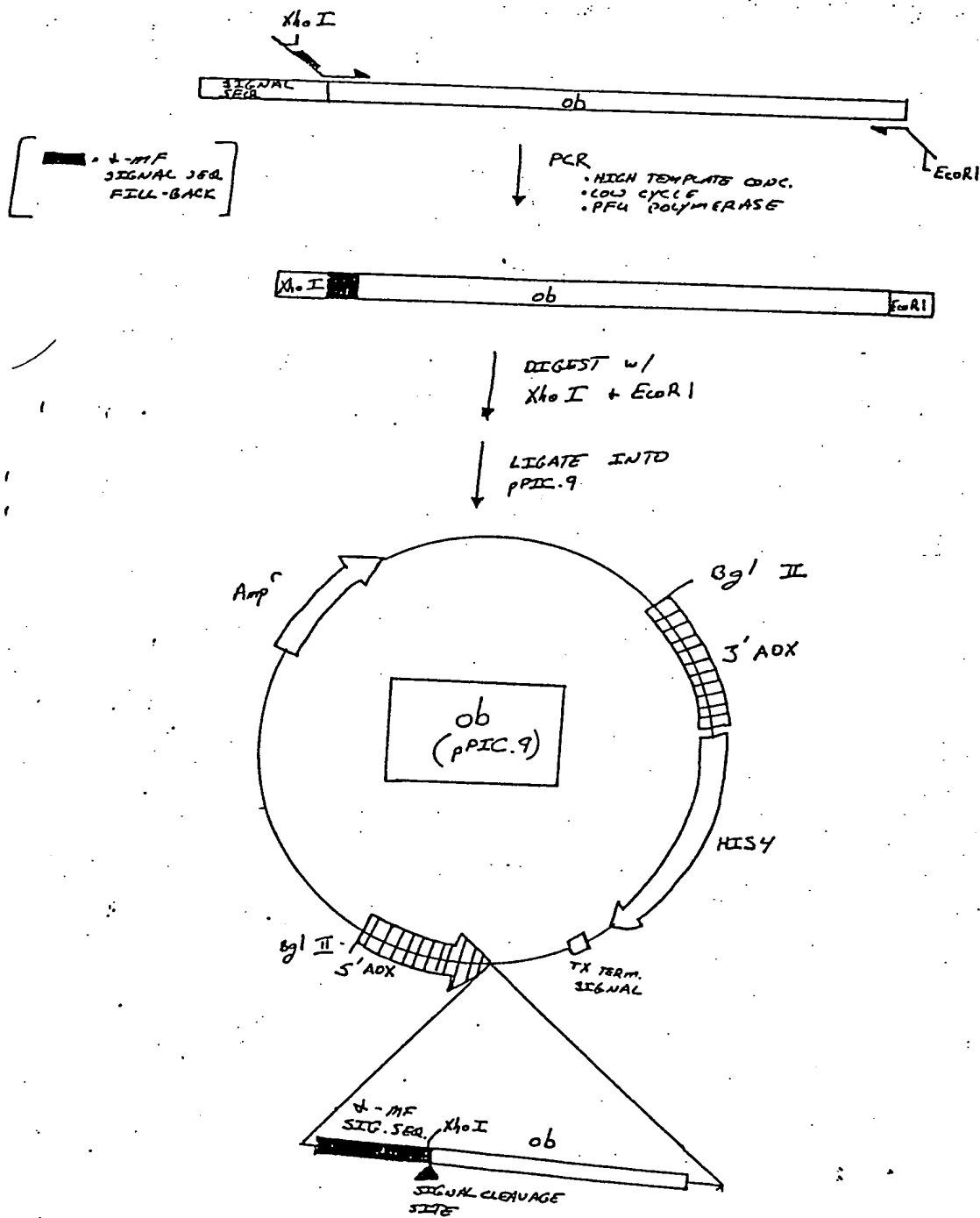


Figure 21 B

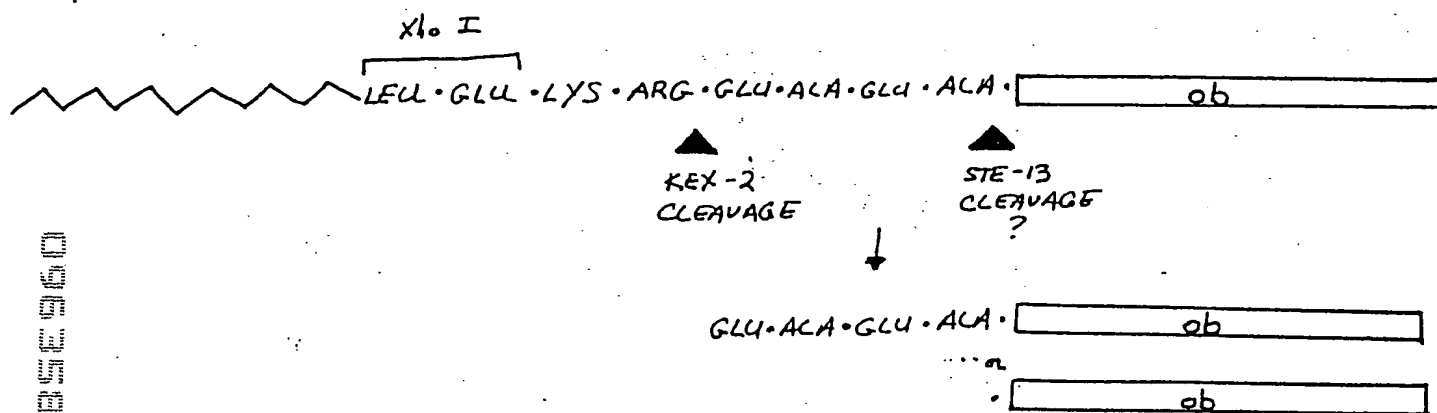


Figure 21 c

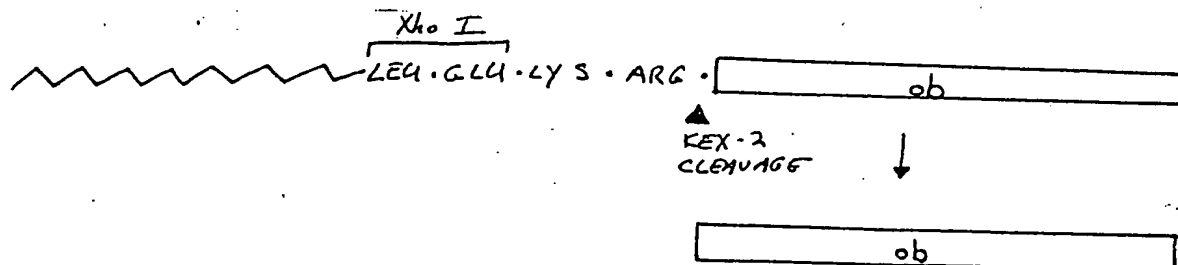
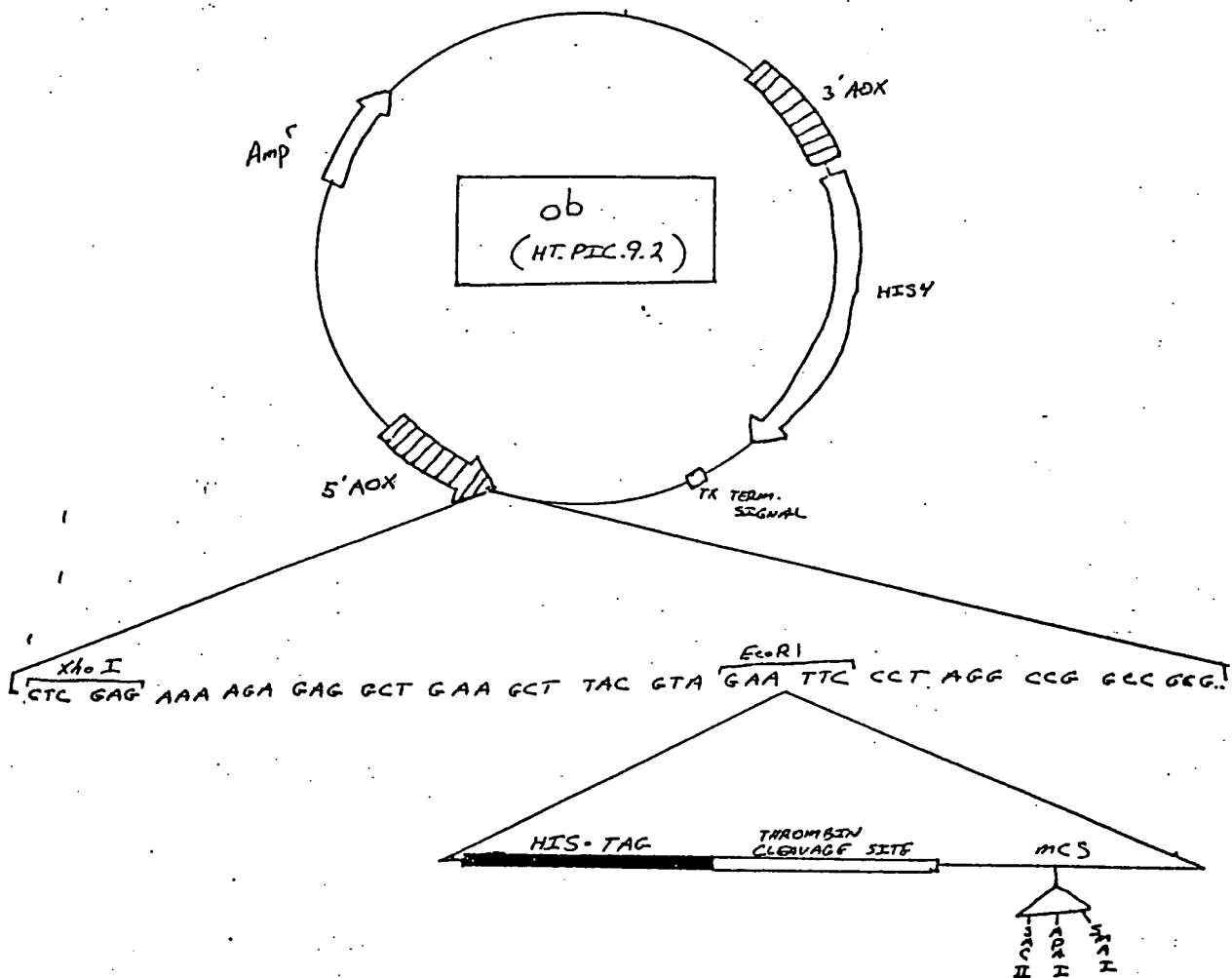


Figure 22A



000730 "49852650

Figure 22B

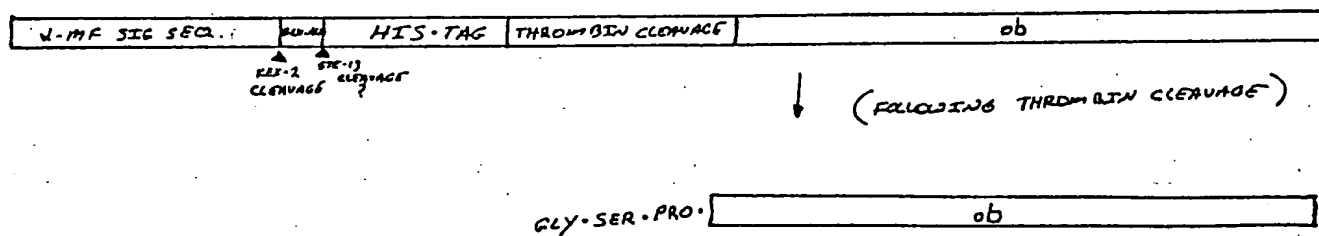


Figure 23A-

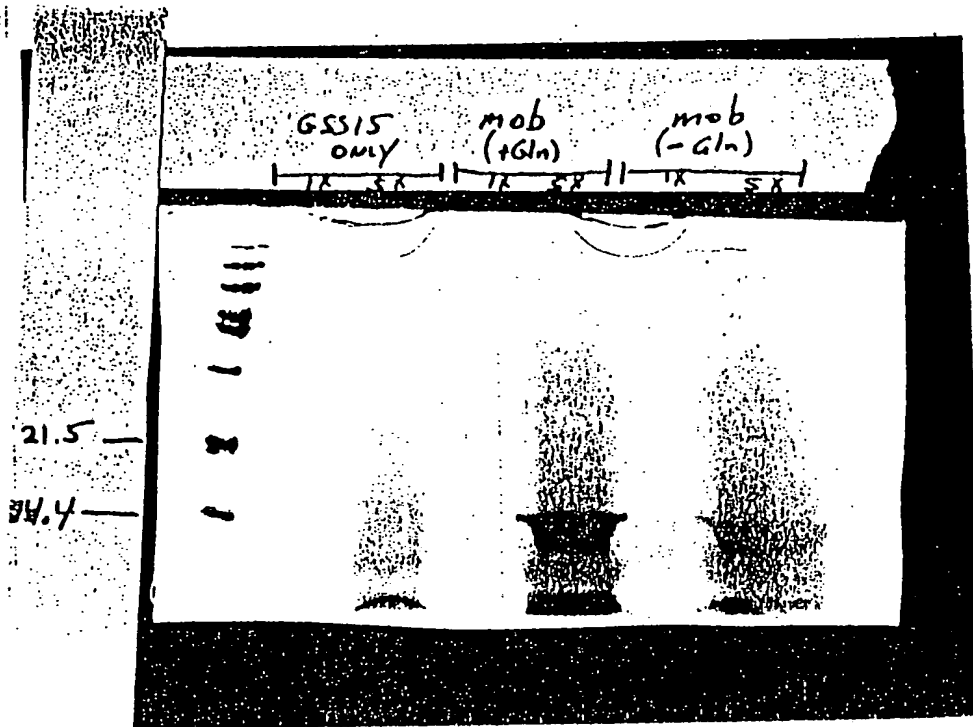
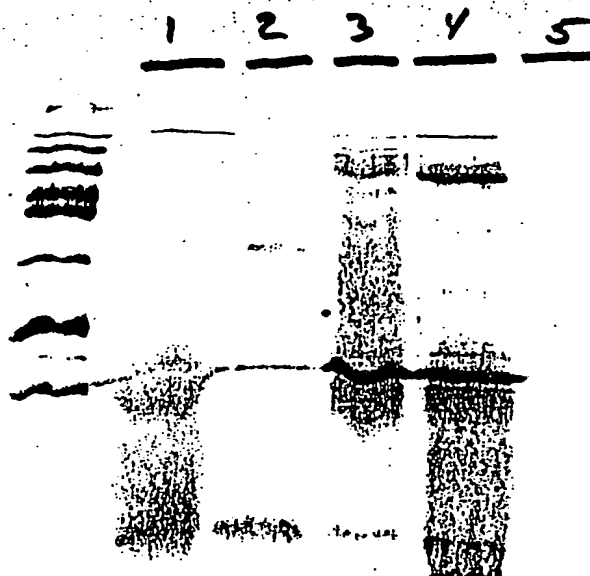
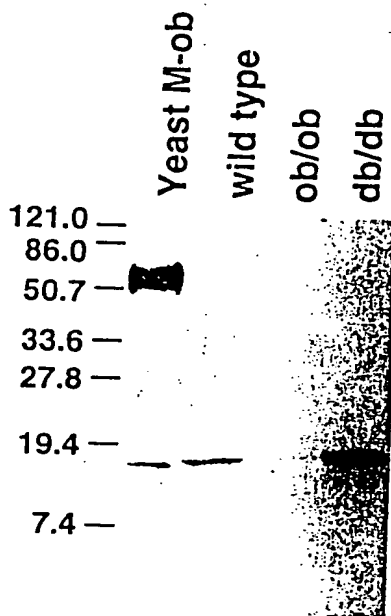


Figure 23 B



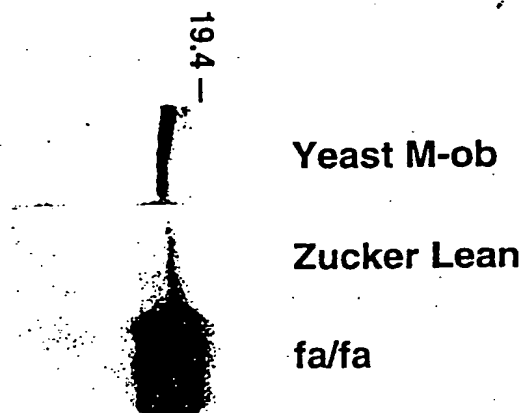
000780"4985E960

Figure 24 A



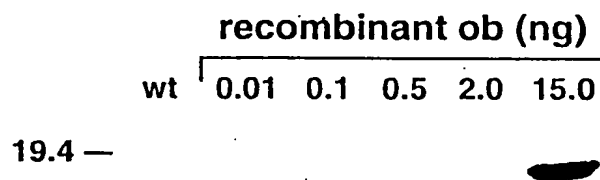
09635864-081000

Figure 24B



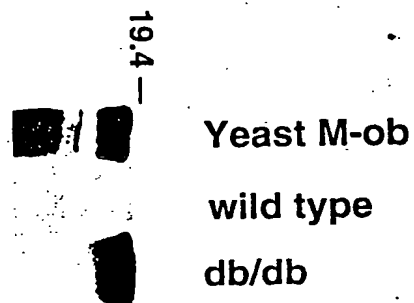
09635864.081000

# Figure 24C



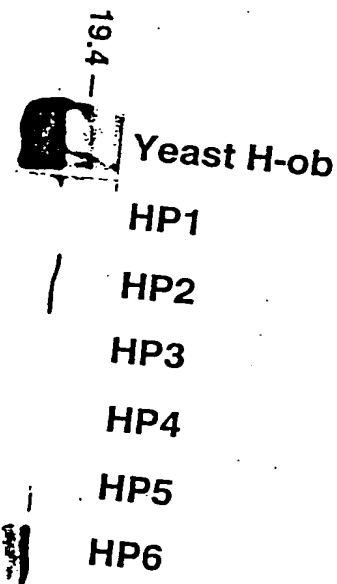
09635864-081000

Figure 24. D



09635864.081000

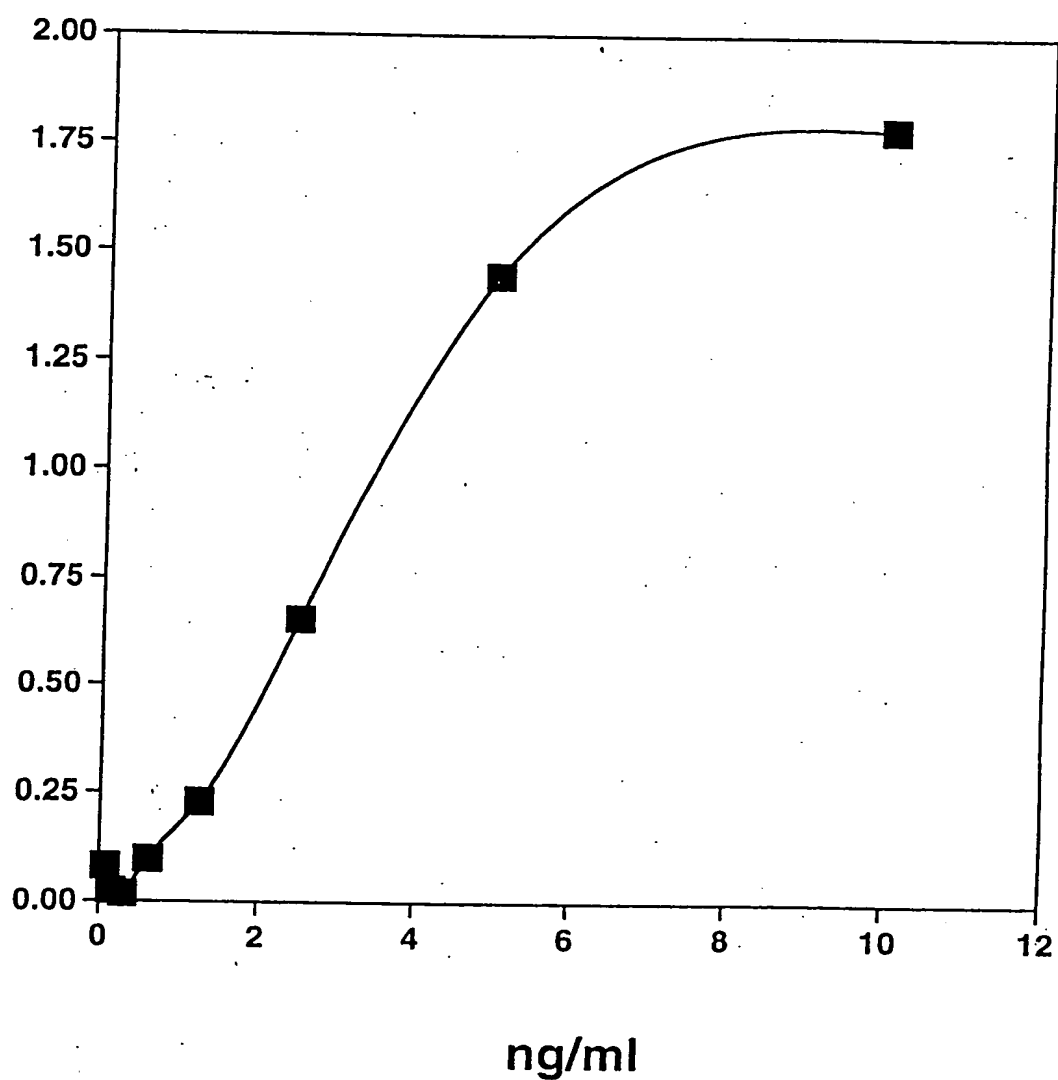
# Figure 25A



09635864.081000

Figure 25 B

## ELISA STANDARD CURVE



## Human ob

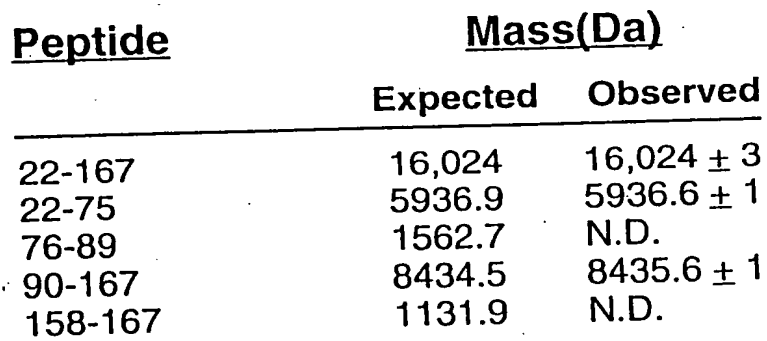


Figure 27



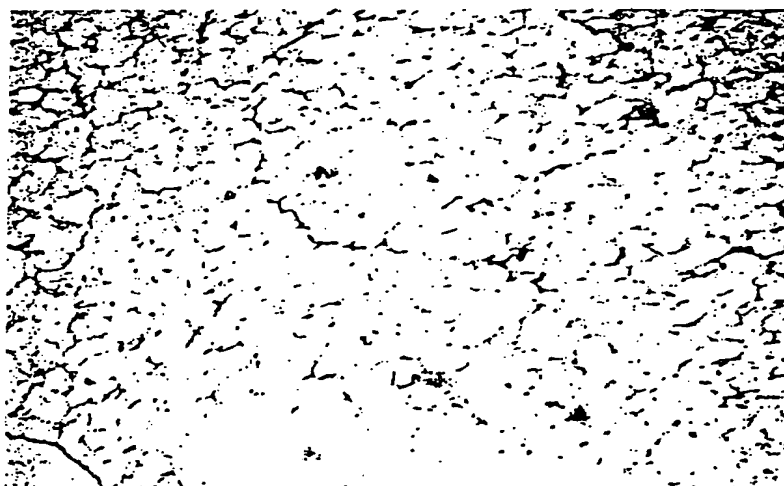


Figure 28D



000780-1985960

Wt



db/db

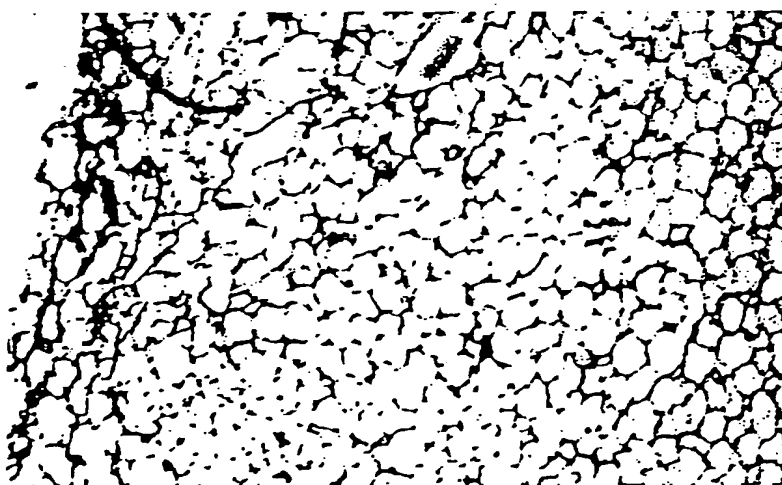
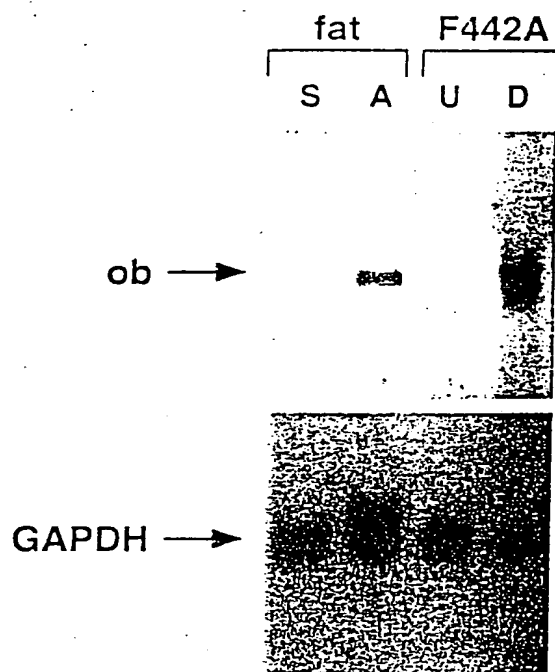
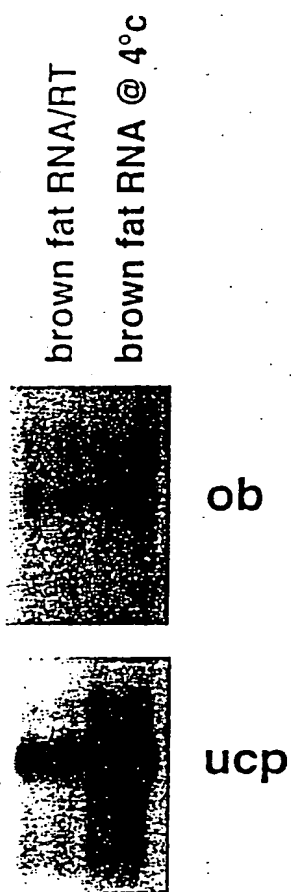


Figure 30



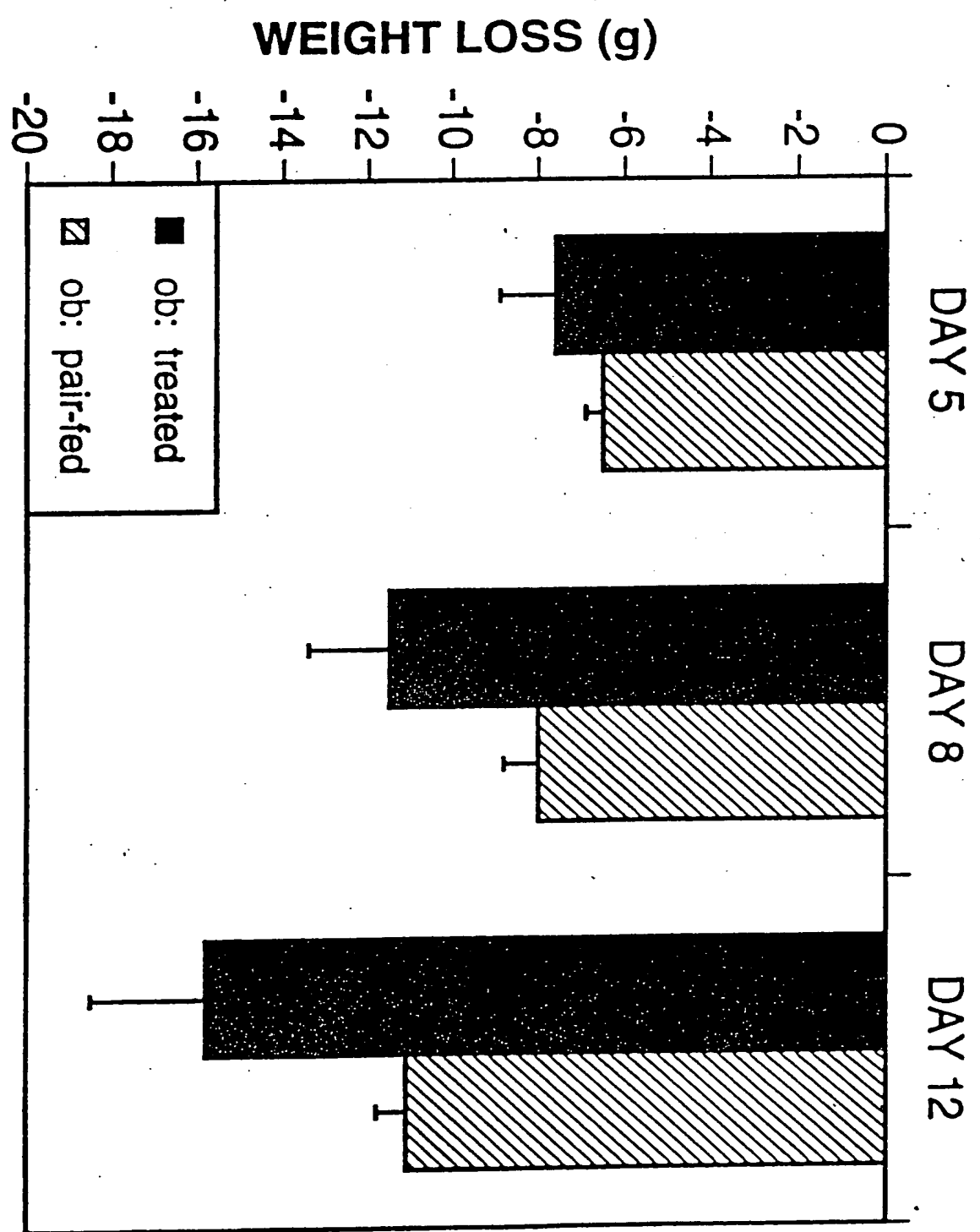
000T80" 1985E960

Figure 31 B



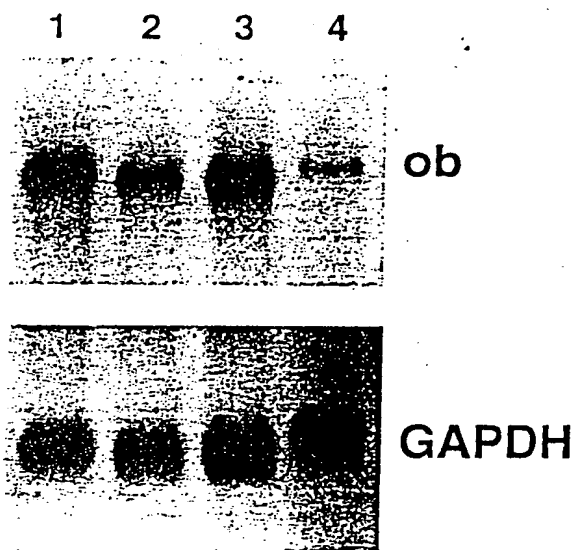
000780" 4985E960

Figure 28B



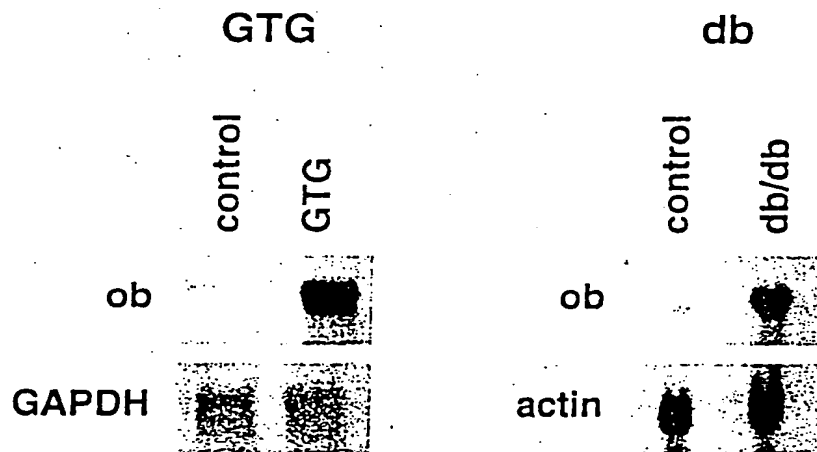
09635864.031000

Figure 31 A



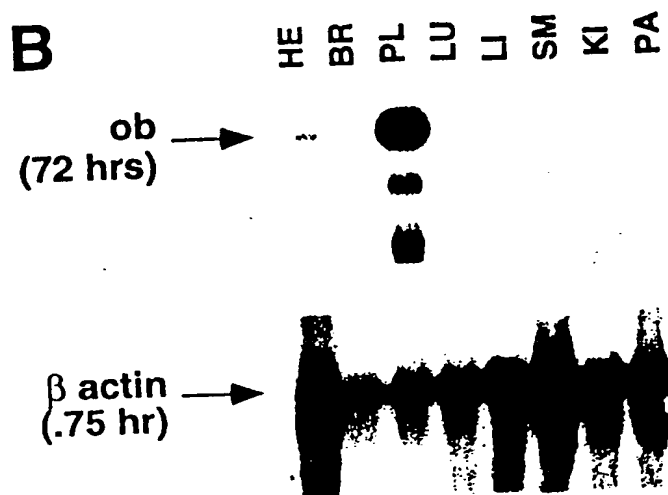
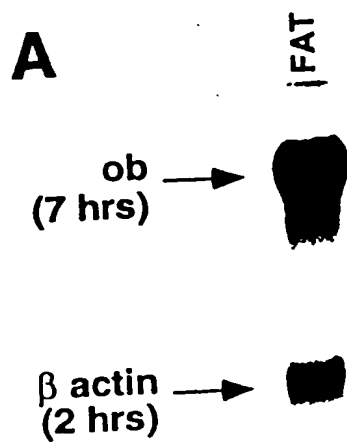
000780"498555960

Figure 32



000780" 4985E960

Figure 33



000780" 49855960

000T80" 14855E960

Figure 34

